

APL-03-04PCT\_Sequence\_Listing  
SEQUENCE LISTING

<110> Aventis Pasteur Limited  
Brunham, Robert  
Raudonikiene, Ausra  
Gallichan, Scott  
Murdin, Andrew

<120> Immunization Against Chlamydia Infectio with 60K CRMP

<130> RY185

<140> US 10/580,141  
<141> 2006-05-19

<150> US 60/481,676  
<151> 2003-11-20

<150> PCT/CA2004/002004  
<151> 2004-11-22

<160> 14

<170> PatentIn version 3.3

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<212> DNA  
<213> Chlamydia muridium

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Ile Phe Ala Val Thr Ser Val Ala Ser Leu Phe Ala Ser Gly Val Leu	
20 25 30	
gag acc tct atg gca gag tct ctc tct acc aac gtt att agc tta gct	144
Glu Thr Ser Met Ala Glu Ser Leu Ser Thr Asn Val Ile Ser Leu Ala	
35 40 45	
gac acc aaa gcg aaa gag acc act tct cat caa aaa gac aga aaa gca	192
Asp Thr Lys Ala Lys Glu Thr Thr Ser His Gln Lys Asp Arg Lys Ala	
50 55 60	
aga aaa aat cat caa aat agg act tcc gta gtc cgt aaa gag gtt act	240
Arg Lys Asn His Gln Asn Arg Thr Ser Val Val Arg Lys Glu Val Thr	
65 70 75 80	
gca gtt cgt gat act aaa gct gta gag cct aga cag gat tct tgc ttt	288
Ala Val Arg Asp Thr Lys Ala Val Glu Pro Arg Gln Asp Ser Cys Phe	
85 90 95	
ggc aaa atg tat aca gtc aaa gtt aat gat gat cgt aat gta gaa atc	336
Gly Lys Met Tyr Thr Val Lys Val Asn Asp Asp Arg Asn Val Glu Ile	

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Glu	Ile	Thr	Ala	Ile	Gly	Lys	Arg	Asp	Cys	Val	Asp	Val	Ile	Ile	Thr			
	130					135					140							
cag	caa	tta	cca	tgc	gaa	gca	gag	ttt	ggt	agc	agt	gat	cca	gct	act			480
Gln	Gln	Leu	Pro	Cys	Glu	Ala	Glu	Phe	Val	Ser	Ser	Asp	Pro	Ala	Thr			
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act	cct	act	gct	gat	ggg	aag	cta	ggt	tgg	aaa	att	gat	cgg	tta	gga			528
Thr	Pro	Thr	Ala	Asp	Gly	Lys	Leu	Val	Trp	Lys	Ile	Asp	Arg	Leu	Gly			
				165					170					175				
cag	ggc	gaa	aag	agt	aaa	att	act	gta	tgg	gta	aaa	cct	ctt	aaa	gaa			576
Gln	Gly	Glu	Lys	Ser	Lys	Ile	Thr	Val	Trp	Val	Lys	Pro	Leu	Lys	Glu			
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ggg	tgc	tgc	ttt	aca	gct	gca	acg	ggt	tgt	gct	tgt	cca	gag	atc	cgt			624
Gly	Cys	Cys	Phe	Thr	Ala	Ala	Thr	Val	Cys	Ala	Cys	Pro	Glu	Ile	Arg			
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tcg	ggt	acg	aaa	tgt	ggc	cag	cct	gct	atc	tgt	ggt	aaa	cag	gaa	ggg			672
Ser	Val	Thr	Lys	Cys	Gly	Gln	Pro	Ala	Ile	Cys	Val	Lys	Gln	Glu	Gly			
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Pro	Glu	Ser	Ala	Cys	Leu	Arg	Cys	Pro	Val	Thr	Tyr	Arg	Ile	Asn	Val			
					230					235					240			
gtc	aac	caa	gga	aca	gca	aca	gca	cgt	aat	ggt	ggt	gtg	gaa	aat	cct			768
Val	Asn	Gln	Gly	Thr	Ala	Thr	Ala	Arg	Asn	Val	Val	Val	Glu	Asn	Pro			
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Val	Pro	Asp	Gly	Tyr	Ala	His	Ala	Ser	Gly	Gln	Arg	Val	Leu	Thr	Tyr			
			260					265					270					
act	ctt	ggg	gat	atg	caa	cct	gga	gaa	cag	aga	aca	atc	acc	gtg	gag			864
Thr	Leu	Gly	Asp	Met	Gln	Pro	Gly	Glu	Gln	Arg	Thr	Ile	Thr	Val	Glu			
		275					280					285						
ttt	tgt	ccg	ctt	aaa	cgt	ggg	cga	gtc	aca	aat	att	gct	aca	ggt	tct			912
Phe	Cys	Pro	Leu	Lys	Arg	Gly	Arg	Val	Thr	Asn	Ile	Ala	Thr	Val	Ser			
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tac	tgt	ggg	gga	cac	aaa	aat	act	gct	agc	gta	aca	aca	gtg	atc	aat			960
Tyr	Cys	Gly	Gly	His	Lys	Asn	Thr	Ala	Ser	Val	Thr	Thr	Val	Ile	Asn			
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gag	cct	tgc	gtg	caa	ggt	aac	atc	gag	gga	gca	gat	tgg	tct	tat	ggt			1008
Glu	Pro	Cys	Val	Gln	Val	Asn	Ile	Glu	Gly	Ala	Asp	Trp	Ser	Tyr	Val			
				325					330					335				
tgt	aag	cct	gta	gaa	tat	ggt	atc	tct	ggt	tct	aac	cct	ggg	gac	tta			1056
Cys	Lys	Pro	Val	Glu	Tyr	Val	Ile	Ser	Val	Ser	Asn	Pro	Gly	Asp	Leu			
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gta	aga	gct	caa	act	cca	ggg	caa	ttc	aca	aac	aac	gtt	gtt	gtg	aaa	1248	
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Ser	Cys	Ser	Asp	Cys	Gly	Ile	Cys	Thr	Ser	Cys	Ala	Glu	Ala	Thr	Thr		
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Tyr	Trp	Lys	Gly	Val	Ala	Ala	Thr	His	Met	Cys	Val	Val	Asp	Thr	Cys		
		435					440					445					
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Asn	Arg	Gly	Ser	Ala	Glu	Asp	Thr	Asn	Val	Ser	Leu	Ile	Leu	Lys	Phe		
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Ser	Lys	Glu	Leu	Gln	Pro	Ile	Ser	Phe	Ser	Gly	Pro	Thr	Lys	Gly	Thr		
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Ile	Thr	Gly	Asn	Thr	Val	Val	Phe	Asp	Ser	Leu	Pro	Arg	Leu	Gly	Ser		
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Lys	Glu	Thr	Val	Glu	Phe	Ser	Val	Thr	Leu	Lys	Ala	Val	Ser	Ala	Gly		
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Asp	Ala	Arg	Gly	Glu	Ala	Ile	Leu	Ser	Ser	Asp	Thr	Leu	Thr	Val	Pro		
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Glu Ile Thr Ala Ile Gly Lys Arg Asp Cys Val Asp Val Ile Ile Thr  
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Gln Gln Leu Pro Cys Glu Ala Glu Phe Val Ser Ser Asp Pro Ala Thr  
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Thr Pro Thr Ala Asp Gly Lys Leu Val Trp Lys Ile Asp Arg Leu Gly  
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Gln Gly Glu Lys Ser Lys Ile Thr Val Trp Val Lys Pro Leu Lys Glu  
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Gly Cys Cys Phe Thr Ala Ala Thr Val Cys Ala Cys Pro Glu Ile Arg  
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Ser Val Thr Lys Cys Gly Gln Pro Ala Ile Cys Val Lys Gln Glu Gly  
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Val Asn Gln Gly Thr Ala Thr Ala Arg Asn Val Val Val Glu Asn Pro  
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Val Pro Asp Gly Tyr Ala His Ala Ser Gly Gln Arg Val Leu Thr Tyr  
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# APL-03-04PCT\_Sequence\_Listing

Thr Leu Gly Asp Met Gln Pro Gly Glu Gln Arg Thr Ile Thr Val Glu  
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 Tyr Cys Gly Gly His Lys Asn Thr Ala Ser Val Thr Thr Val Ile Asn  
 305 310 315 320  
 Glu Pro Cys Val Gln Val Asn Ile Glu Gly Ala Asp Trp Ser Tyr Val  
 325 330 335  
 Cys Lys Pro Val Glu Tyr Val Ile Ser Val Ser Asn Pro Gly Asp Leu  
 340 345 350  
 Val Leu Arg Asp Val Val Ile Glu Asp Thr Leu Ser Pro Gly Ile Thr  
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 Val Val Glu Ala Ala Gly Ala Gln Ile Ser Cys Asn Lys Leu Val Trp  
 370 375 380  
 Thr Leu Lys Glu Leu Asn Pro Gly Glu Ser Leu Gln Tyr Lys Val Leu  
 385 390 395 400  
 Val Arg Ala Gln Thr Pro Gly Gln Phe Thr Asn Asn Val Val Val Lys  
 405 410 415  
 Ser Cys Ser Asp Cys Gly Ile Cys Thr Ser Cys Ala Glu Ala Thr Thr  
 420 425 430  
 Tyr Trp Lys Gly Val Ala Ala Thr His Met Cys Val Val Asp Thr Cys  
 435 440 445  
 Asp Pro Ile Cys Val Gly Glu Asn Thr Val Tyr Arg Ile Cys Val Thr  
 450 455 460  
 Asn Arg Gly Ser Ala Glu Asp Thr Asn Val Ser Leu Ile Leu Lys Phe  
 465 470 475 480  
 Ser Lys Glu Leu Gln Pro Ile Ser Phe Ser Gly Pro Thr Lys Gly Thr  
 485 490 495  
 Ile Thr Gly Asn Thr Val Val Phe Asp Ser Leu Pro Arg Leu Gly Ser  
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 Lys Glu Thr Val Glu Phe Ser Val Thr Leu Lys Ala Val Ser Ala Gly  
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# APL-03-04PCT\_Sequence\_Listing

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Ile Phe Ala Val Thr Ser Val Ala Ser Leu Phe Ala Ser Gly Val Leu	
20 25 30	
gag acc tct atg gca gag tct ctc tct aca aac gtt att agc tta gct	144
Glu Thr Ser Met Ala Glu Ser Leu Ser Thr Asn Val Ile Ser Leu Ala	
35 40 45	
gac acc aaa gcg aaa gac aac act tct cat aaa agc aaa aaa gca aga	192
Asp Thr Lys Ala Lys Asp Asn Thr Ser His Lys Ser Lys Lys Ala Arg	
50 55 60	
aaa aac cac agc aaa gag act ccc gta gac cgt aaa gag gtt gct ccg	240
Lys Asn His Ser Lys Glu Thr Pro Val Asp Arg Lys Glu Val Ala Pro	
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gtt cat gag tct aaa gct aca gga cct aaa cag gat tct tgc ttt ggc	288
Val His Glu Ser Lys Ala Thr Gly Pro Lys Gln Asp Ser Cys Phe Gly	
85 90 95	
aga atg tat aca gtc aaa gtt aat gat gat cgc aat gtt gaa atc aca	336
Arg Met Tyr Thr Val Lys Val Asn Asp Asp Arg Asn Val Glu Ile Thr	
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caa gct gtt cct gaa tat gct acg gta gga tct ccc tat cct att gaa	384
Gln Ala Val Pro Glu Tyr Ala Thr Val Gly Ser Pro Tyr Pro Ile Glu	
115 120 125	
att act gct aca ggt aaa agg gat tgt gtt gat gtt atc att act cag	432
Ile Thr Ala Thr Gly Lys Arg Asp Cys Val Asp Val Ile Ile Thr Gln	
130 135 140	
caa tta cca tgt gaa gca gag ttc gta cgc agt gat cca gcg aca act	480
Gln Leu Pro Cys Glu Ala Glu Phe Val Arg Ser Asp Pro Ala Thr Thr	
145 150 155 160	
cct act gct gat ggt aag cta gtt tgg aaa att gac cgc tta gga caa	528
Pro Thr Ala Asp Gly Lys Leu Val Trp Lys Ile Asp Arg Leu Gly Gln	

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Gly	Glu	Lys	Ser	Lys	Ile	Thr	Val	Trp	Val	Lys	Pro	Leu	Lys	Glu	Gly	
				180					185					190		
tgc	tgc	ttt	aca	gct	gca	aca	gta	tgc	gct	tgt	cca	gag	atc	cgt	tcg	624
Cys	Cys	Phe	Thr	Ala	Ala	Thr	Val	Cys	Ala	Cys	Pro	Glu	Ile	Arg	Ser	
				195					200					205		
gtt	aca	aaa	tgt	gga	caa	cct	gct	atc	tgt	gtt	aaa	caa	gaa	ggc	cca	672
Val	Thr	Lys	Cys	Gly	Gln	Pro	Ala	Ile	Cys	Val	Lys	Gln	Glu	Gly	Pro	
				210					215					220		
gag	aat	gct	tgt	ttg	cgt	tgc	cca	gta	gtt	tac	aaa	att	aat	ata	gtg	720
Glu	Asn	Ala	Cys	Leu	Arg	Cys	Pro	Val	Val	Tyr	Lys	Ile	Asn	Ile	Val	
				225					230					235		
aac	caa	gga	aca	gca	aca	gct	cgt	aac	gtt	gtt	gtt	gaa	aat	cct	gtt	768
Asn	Gln	Gly	Thr	Ala	Thr	Ala	Arg	Asn	Val	Val	Val	Glu	Asn	Pro	Val	
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cca	gat	ggc	tac	gct	cat	tct	tct	gga	cag	cgt	gta	ctg	acg	ttt	act	816
Pro	Asp	Gly	Tyr	Ala	His	Ser	Ser	Gly	Gln	Arg	Val	Leu	Thr	Phe	Thr	
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ctt	gga	gat	atg	caa	cct	gga	gag	cac	aga	aca	att	act	gta	gag	ttt	864
Leu	Gly	Asp	Met	Gln	Pro	Gly	Glu	His	Arg	Thr	Ile	Thr	Val	Glu	Phe	
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tgt	ccg	ctt	aaa	cgt	ggc	cgt	gct	acc	aat	ata	gca	acg	gtt	tct	tac	912
Cys	Pro	Leu	Lys	Arg	Gly	Arg	Ala	Thr	Asn	Ile	Ala	Thr	Val	Ser	Tyr	
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Cys	Gly	Gly	His	Lys	Asn	Thr	Ala	Ser	Val	Thr	Thr	Val	Ile	Asn	Glu	
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cct	tgc	gta	caa	gta	agt	att	gca	gga	gca	gat	tgg	tct	tat	gtt	tgt	1008
Pro	Cys	Val	Gln	Val	Ser	Ile	Ala	Gly	Ala	Asp	Trp	Ser	Tyr	Val	Cys	
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aag	cct	gta	gaa	tat	gtg	atc	tcc	gtt	tcc	aat	cct	gga	gat	ctt	gtg	1056
Lys	Pro	Val	Glu	Tyr	Val	Ile	Ser	Val	Ser	Asn	Pro	Gly	Asp	Leu	Val	
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ttg	cga	gat	gtc	gtc	gtt	gaa	gac	act	ctt	tct	ccc	gga	gtc	aca	gtt	1104
Leu	Arg	Asp	Val	Val	Val	Glu	Asp	Thr	Leu	Ser	Pro	Gly	Val	Thr	Val	
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Leu	Glu	Ala	Ala	Gly	Ala	Gln	Ile	Ser	Cys	Asn	Lys	Val	Val	Trp	Thr	
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gtg	aaa	gaa	ctg	aat	cct	gga	gag	tct	cta	cag	tat	aaa	gtt	cta	gta	1200
Val	Lys	Glu	Leu	Asn	Pro	Gly	Glu	Ser	Leu	Gln	Tyr	Lys	Val	Leu	Val	
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aga	gca	caa	act	cct	gga	caa	ttc	aca	aat	aat	gtt	gtt	gtg	aag	agc	1248
Arg	Ala	Gln	Thr	Pro	Gly	Gln	Phe	Thr	Asn	Asn	Val	Val	Val	Lys	Ser	
				405					410					415		
tgc	tct	gac	tgt	ggc	act	tgt	act	tct	tgc	gca	gaa	gcg	aca	act	tac	1296

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Cys	Ser	Asp	Cys 420	Gly	Thr	Cys	Thr	Ser 425	Cys	Ala	Glu	Ala	Thr 430	Thr	Tyr		
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Trp	Lys	Gly 435	Val	Ala	Ala	Thr	His 440	Met	Cys	Val	Val	Asp 445	Thr	Cys	Asp		
cct	gtt	tgt	gta	gga	gaa	aat	act	gtt	tac	cgt	att	tgt	gtc	acc	aac	1392	
Pro	Val 450	Cys	Val	Gly	Glu	Asn 455	Thr	Val	Tyr	Arg	Ile 460	Cys	Val	Thr	Asn		
aga	ggt	tct	gca	gaa	gat	aca	aat	gtt	tct	tta	atg	ctt	aaa	ttc	tct	1440	
Arg 465	Gly	Ser	Ala	Glu	Asp 470	Thr	Asn	Val	Ser	Leu 475	Met	Leu	Lys	Phe	Ser 480		
aaa	gaa	ctg	caa	cct	gta	tcc	ttc	tct	gga	cca	act	aaa	gga	acg	att	1488	
Lys	Glu	Leu	Gln 485	Pro	Val	Ser	Phe	Ser	Gly 490	Pro	Thr	Lys	Gly	Thr 495	Ile		
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Thr	Gly	Asn 500	Thr	Val	Val	Phe	Asp	Ser 505	Leu	Pro	Arg	Leu	Gly 510	Ser	Lys		
gaa	act	gta	gag	ttt	tct	gta	aca	ttg	aaa	gca	gta	tca	gct	gga	gat	1584	
Glu	Thr	Val 515	Glu	Phe	Ser	Val	Thr 520	Leu	Lys	Ala	Val	Ser 525	Ala	Gly	Asp		
gct	cgt	ggg	gaa	gcg	att	ctt	tct	tcc	gat	aca	ttg	act	gtt	cca	gtt	1632	
Ala	Arg 530	Gly	Glu	Ala	Ile	Leu 535	Ser	Ser	Asp	Thr	Leu 540	Thr	Val	Pro	Val		
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Ser	Asp	Thr	Glu	Asn 550	Thr	His	Ile	Tyr									

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Glu	Thr	Ser	Met	Ala	Glu	Ser	Leu	Ser	Thr	Asn	Val	Ile	Ser	Leu	Ala
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Asp	Thr	Lys	Ala	Lys	Asp	Asn	Thr	Ser	His	Lys	Ser	Lys	Lys	Ala	Arg
	50					55					60				
Lys	Asn	His	Ser	Lys	Glu	Thr	Pro	Val	Asp	Arg	Lys	Glu	Val	Ala	Pro
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Val His Glu Ser Lys Ala Thr Gly Pro Lys Gln Asp Ser Cys Phe Gly  
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 115 120 125  
 Ile Thr Ala Thr Gly Lys Arg Asp Cys Val Asp Val Ile Ile Thr Gln  
 130 135 140  
 Gln Leu Pro Cys Glu Ala Glu Phe Val Arg Ser Asp Pro Ala Thr Thr  
 145 150 155 160  
 Pro Thr Ala Asp Gly Lys Leu Val Trp Lys Ile Asp Arg Leu Gly Gln  
 165 170 175  
 Gly Glu Lys Ser Lys Ile Thr Val Trp Val Lys Pro Leu Lys Glu Gly  
 180 185 190  
 Cys Cys Phe Thr Ala Ala Thr Val Cys Ala Cys Pro Glu Ile Arg Ser  
 195 200 205  
 Val Thr Lys Cys Gly Gln Pro Ala Ile Cys Val Lys Gln Glu Gly Pro  
 210 215 220  
 Glu Asn Ala Cys Leu Arg Cys Pro Val Val Tyr Lys Ile Asn Ile Val  
 225 230 235 240  
 Asn Gln Gly Thr Ala Thr Ala Arg Asn Val Val Val Glu Asn Pro Val  
 245 250 255  
 Pro Asp Gly Tyr Ala His Ser Ser Gly Gln Arg Val Leu Thr Phe Thr  
 260 265 270  
 Leu Gly Asp Met Gln Pro Gly Glu His Arg Thr Ile Thr Val Glu Phe  
 275 280 285  
 Cys Pro Leu Lys Arg Gly Arg Ala Thr Asn Ile Ala Thr Val Ser Tyr  
 290 295 300  
 Cys Gly Gly His Lys Asn Thr Ala Ser Val Thr Thr Val Ile Asn Glu  
 305 310 315 320  
 Pro Cys Val Gln Val Ser Ile Ala Gly Ala Asp Trp Ser Tyr Val Cys  
 325 330 335

# APL-03-04PCT\_Sequence\_Listing

Lys Pro Val Glu Tyr Val Ile Ser Val Ser Asn Pro Gly Asp Leu Val  
340 345 350

Leu Arg Asp Val Val Val Glu Asp Thr Leu Ser Pro Gly Val Thr Val  
355 360 365

Leu Glu Ala Ala Gly Ala Gln Ile Ser Cys Asn Lys Val Val Trp Thr  
370 375 380

Val Lys Glu Leu Asn Pro Gly Glu Ser Leu Gln Tyr Lys Val Leu Val  
385 390 395 400

Arg Ala Gln Thr Pro Gly Gln Phe Thr Asn Asn Val Val Val Lys Ser  
405 410 415

Cys Ser Asp Cys Gly Thr Cys Thr Ser Cys Ala Glu Ala Thr Thr Tyr  
420 425 430

Trp Lys Gly Val Ala Ala Thr His Met Cys Val Val Asp Thr Cys Asp  
435 440 445

Pro Val Cys Val Gly Glu Asn Thr Val Tyr Arg Ile Cys Val Thr Asn  
450 455 460

Arg Gly Ser Ala Glu Asp Thr Asn Val Ser Leu Met Leu Lys Phe Ser  
465 470 475 480

Lys Glu Leu Gln Pro Val Ser Phe Ser Gly Pro Thr Lys Gly Thr Ile  
485 490 495

Thr Gly Asn Thr Val Val Phe Asp Ser Leu Pro Arg Leu Gly Ser Lys  
500 505 510

Glu Thr Val Glu Phe Ser Val Thr Leu Lys Ala Val Ser Ala Gly Asp  
515 520 525

Ala Arg Gly Glu Ala Ile Leu Ser Ser Asp Thr Leu Thr Val Pro Val  
530 535 540

Ser Asp Thr Glu Asn Thr His Ile Tyr  
545 550

<210> 5  
<211> 1554  
<212> DNA  
<213> Chlamydia muridum

# APL-03-04PCT\_Sequence\_Listing

<220>

<221> CDS

<222> (1)..(1554)

<400> 5

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Met	Glu	Ser	Leu	Ser	Thr	Asn	Val	Ile	Ser	Leu	Ala	Asp	Thr	Lys	Ala	
1				5					10					15		

aaa	gag	acc	act	tct	cat	caa	aaa	gac	aga	aaa	gca	aga	aaa	aat	cat	96
Lys	Glu	Thr	Thr	Ser	His	Gln	Lys	Asp	Arg	Lys	Ala	Arg	Lys	Asn	His	
			20					25					30			

caa	aat	agg	act	tcc	gta	gtc	cgt	aaa	gag	ggt	act	gca	ggt	cgt	gat	144
Gln	Asn	Arg	Thr	Ser	Val	Val	Arg	Lys	Glu	Val	Thr	Ala	Val	Arg	Asp	
		35					40					45				

act	aaa	gct	gta	gag	cct	aga	cag	gat	tct	tgc	ttt	ggc	aaa	atg	tat	192
Thr	Lys	Ala	Val	Glu	Pro	Arg	Gln	Asp	Ser	Cys	Phe	Gly	Lys	Met	Tyr	
	50					55					60					

aca	gtc	aaa	ggt	aat	gat	gat	cgt	aat	gta	gaa	atc	gtg	cag	tcc	ggt	240
Thr	Val	Lys	Val	Asn	Asp	Asp	Arg	Asn	Val	Glu	Ile	Val	Gln	Ser	Val	
65				70					75						80	

cct	gaa	tat	gct	acg	gta	gga	tct	cca	tat	cct	att	gag	att	act	gct	288
Pro	Glu	Tyr	Ala	Thr	Val	Gly	Ser	Pro	Tyr	Pro	Ile	Glu	Ile	Thr	Ala	
				85					90					95		

ata	ggg	aaa	aga	gac	tgt	ggt	gat	gta	atc	att	aca	cag	caa	tta	cca	336
Ile	Gly	Lys	Arg	Asp	Cys	Val	Asp	Val	Ile	Ile	Thr	Gln	Gln	Leu	Pro	
			100					105					110			

tgc	gaa	gca	gag	ttt	ggt	agc	agt	gat	cca	gct	act	act	cct	act	gct	384
Cys	Glu	Ala	Glu	Phe	Val	Ser	Ser	Asp	Pro	Ala	Thr	Thr	Pro	Thr	Ala	
		115					120					125				

gat	ggt	aag	cta	ggt	tgg	aaa	att	gat	cgg	tta	gga	cag	ggc	gaa	aag	432
Asp	Gly	Lys	Leu	Val	Trp	Lys	Ile	Asp	Arg	Leu	Gly	Gln	Gly	Glu	Lys	
	130					135					140					

agt	aaa	att	act	gta	tgg	gta	aaa	cct	ctt	aaa	gaa	ggt	tgc	tgc	ttt	480
Ser	Lys	Ile	Thr	Val	Trp	Val	Lys	Pro	Leu	Lys	Glu	Gly	Cys	Cys	Phe	
145				150					155						160	

aca	gct	gca	acg	ggt	tgt	gct	tgt	cca	gag	atc	cgt	tcg	ggt	acg	aaa	528
Thr	Ala	Ala	Thr	Val	Cys	Ala	Cys	Pro	Glu	Ile	Arg	Ser	Val	Thr	Lys	
				165					170					175		

tgt	ggc	cag	cct	gct	atc	tgt	ggt	aaa	cag	gaa	ggt	cca	gaa	agc	gca	576
Cys	Gly	Gln	Pro	Ala	Ile	Cys	Val	Lys	Gln	Glu	Gly	Pro	Glu	Ser	Ala	
			180					185					190			

tgt	ttg	cgt	tgc	cca	gta	act	tat	aga	att	aat	gta	gtc	aac	caa	gga	624
Cys	Leu	Arg	Cys	Pro	Val	Thr	Tyr	Arg	Ile	Asn	Val	Val	Asn	Gln	Gly	
		195					200					205				

aca	gca	aca	gca	cgt	aat	ggt	ggt	gtg	gaa	aat	cct	ggt	cca	gat	ggc	672
Thr	Ala	Thr	Ala	Arg	Asn	Val	Val	Val	Glu	Asn	Pro	Val	Pro	Asp	Gly	
	210					215					220					

tat	gct	cat	gca	tcc	gga	cag	cgt	gta	ttg	aca	tat	act	ctt	ggg	gat	720
Tyr	Ala	His	Ala	Ser	Gly	Gln	Arg	Val	Leu	Thr	Tyr	Thr	Leu	Gly	Asp	

APL-03-04PCT\_Sequence\_Listing

225											230											235											240	
atg	caa	cct	gga	gaa	cag	aga	aca	atc	acc	gtg	gag	ttt	tgt	ccg	ctt																			768
Met	Gln	Pro	Gly	Glu	Gln	Arg	Thr	Ile	Thr	Val	Glu	Phe	Cys	Pro	Leu																			
				245					250					255																				
aaa	cgt	ggt	cga	gtc	aca	aat	att	gct	aca	ggt	tct	tac	tgt	ggt	gga																			816
Lys	Arg	Gly	Arg	Val	Thr	Asn	Ile	Ala	Thr	Val	Ser	Tyr	Cys	Gly	Gly																			
			260					265					270																					
cac	aaa	aat	act	gct	agc	gta	aca	aca	gtg	atc	aat	gag	cct	tgc	gtg																			864
His	Lys	Asn	Thr	Ala	Ser	Val	Thr	Thr	Val	Ile	Asn	Glu	Pro	Cys	Val																			
		275					280					285																						
caa	ggt	aac	atc	gag	gga	gca	gat	tgg	tct	tat	ggt	tgt	aag	cct	gta																			912
Gln	Val	Asn	Ile	Glu	Gly	Ala	Asp	Trp	Ser	Tyr	Val	Cys	Lys	Pro	Val																			
	290					295					300																							
gaa	tat	ggt	atc	tct	ggt	tct	aac	cct	ggt	gac	tta	ggt	tta	cga	gac																			960
Glu	Tyr	Val	Ile	Ser	Val	Ser	Asn	Pro	Gly	Asp	Leu	Val	Leu	Arg	Asp																			
305				310					315					320																				
ggt	gta	att	gaa	gat	acg	ctt	tct	cct	gga	ata	act	ggt	ggt	gaa	gca																			1008
Val	Val	Ile	Glu	Asp	Thr	Leu	Ser	Pro	Gly	Ile	Thr	Val	Val	Glu	Ala																			
			325					330						335																				
gct	gga	gct	cag	att	tct	tgt	aat	aaa	ttg	ggt	tgg	act	ttg	aag	gaa																			1056
Ala	Gly	Ala	Gln	Ile	Ser	Cys	Asn	Lys	Leu	Val	Trp	Thr	Leu	Lys	Glu																			
			340					345					350																					
ctc	aat	cct	gga	gag	tct	tta	caa	tat	aag	ggt	cta	gta	aga	gct	caa																			1104
Leu	Asn	Pro	Gly	Glu	Ser	Leu	Gln	Tyr	Lys	Val	Leu	Val	Arg	Ala	Gln																			
		355					360					365																						
act	cca	ggg	caa	ttc	aca	aac	aac	ggt	ggt	gtg	aaa	agt	tgc	tct	gat																			1152
Thr	Pro	Gly	Gln	Phe	Thr	Asn	Asn	Val	Val	Val	Lys	Ser	Cys	Ser	Asp																			
	370					375					380																							
tgc	ggt	att	tgt	act	tct	tgc	gca	gaa	gca	aca	act	tac	tgg	aaa	gga																			1200
Cys	Gly	Ile	Cys	Thr	Ser	Cys	Ala	Glu	Ala	Thr	Thr	Tyr	Trp	Lys	Gly																			
385				390					395					400																				
ggt	gct	gct	act	cat	atg	tgc	gta	gta	gat	act	tgt	gat	cct	att	tgc																			1248
Val	Ala	Ala	Thr	His	Met	Cys	Val	Val	Asp	Thr	Cys	Asp	Pro	Ile	Cys																			
			405					410						415																				
gta	gga	gag	aac	act	ggt	tat	cgt	atc	tgt	gtg	aca	aac	aga	ggt	tct																			1296
Val	Gly	Glu	Asn	Thr	Val	Tyr	Arg	Ile	Cys	Val	Thr	Asn	Arg	Gly	Ser																			
			420				425						430																					
gct	gaa	gat	aca	aat	gtg	tcc	tta	att	ttg	aaa	ttc	tct	aaa	gaa	tta																			1344
Ala	Glu	Asp	Thr	Asn	Val	Ser	Leu	Ile	Leu	Lys	Phe	Ser	Lys	Glu	Leu																			
		435				440						445																						
caa	cct	ata	tct	ttc	tct	gga	cca	act	aaa	gga	acc	att	aca	gga	aac																			1392
Gln	Pro	Ile	Ser	Phe	Ser	Gly	Pro	Thr	Lys	Gly	Thr	Ile	Thr	Gly	Asn																			
	450					455					460																							
acg	gta	gtg	ttt	gat	tcg	tta	cct	aga	tta	ggt	tct	aaa	gaa	act	gta																			1440
Thr	Val	Val	Phe	Asp	Ser	Leu	Pro	Arg	Leu	Gly	Ser	Lys	Glu	Thr	Val																			
465				470						475				480																				
gag	ttt	tct	gta	acg	ttg	aaa	gca	gta	tcc	gct	gga	gat	gct	cgt	ggg																			1488

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Glu	Phe	Ser	Val	Thr	Leu	Lys	Ala	Val	Ser	Ala	Gly	Asp	Ala	Arg	Gly	
				485					490					495		
gaa	gct	att	ctt	tct	tcc	gat	aca	ttg	aca	gtt	cct	gta	tct	gat	acg	1536
Glu	Ala	Ile	Leu	Ser	Ser	Asp	Thr	Leu	Thr	Val	Pro	Val	Ser	Asp	Thr	
			500					505					510			
gag	aat	aca	cat	atc	tat											1554
Glu	Asn	Thr	His	Ile	Tyr											
			515													

<210> 6  
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 <212> PRT  
 <213> CHlamydia muridium

<400> 6

Met	Glu	Ser	Leu	Ser	Thr	Asn	Val	Ile	Ser	Leu	Ala	Asp	Thr	Lys	Ala	
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Lys	Glu	Thr	Thr	Ser	His	Gln	Lys	Asp	Arg	Lys	Ala	Arg	Lys	Asn	His	
			20					25					30			
Gln	Asn	Arg	Thr	Ser	Val	Val	Arg	Lys	Glu	Val	Thr	Ala	Val	Arg	Asp	
		35					40					45				
Thr	Lys	Ala	Val	Glu	Pro	Arg	Gln	Asp	Ser	Cys	Phe	Gly	Lys	Met	Tyr	
	50					55					60					
Thr	Val	Lys	Val	Asn	Asp	Asp	Arg	Asn	Val	Glu	Ile	Val	Gln	Ser	Val	
65				70						75				80		
Pro	Glu	Tyr	Ala	Thr	Val	Gly	Ser	Pro	Tyr	Pro	Ile	Glu	Ile	Thr	Ala	
				85					90					95		
Ile	Gly	Lys	Arg	Asp	Cys	Val	Asp	Val	Ile	Ile	Thr	Gln	Gln	Leu	Pro	
			100					105					110			
Cys	Glu	Ala	Glu	Phe	Val	Ser	Ser	Asp	Pro	Ala	Thr	Thr	Pro	Thr	Ala	
		115					120					125				
Asp	Gly	Lys	Leu	Val	Trp	Lys	Ile	Asp	Arg	Leu	Gly	Gln	Gly	Glu	Lys	
	130					135					140					
Ser	Lys	Ile	Thr	Val	Trp	Val	Lys	Pro	Leu	Lys	Glu	Gly	Cys	Cys	Phe	
145					150					155					160	
Thr	Ala	Ala	Thr	Val	Cys	Ala	Cys	Pro	Glu	Ile	Arg	Ser	Val	Thr	Lys	
				165					170					175		

APL-03-04PCT\_Sequence\_Listing

Cys Gly Gln Pro Ala Ile Cys Val Lys Gln Glu Gly Pro Glu Ser Ala  
180 185 190

Cys Leu Arg Cys Pro Val Thr Tyr Arg Ile Asn Val Val Asn Gln Gly  
195 200 205

Thr Ala Thr Ala Arg Asn Val Val Val Glu Asn Pro Val Pro Asp Gly  
210 215 220

Tyr Ala His Ala Ser Gly Gln Arg Val Leu Thr Tyr Thr Leu Gly Asp  
225 230 235 240

Met Gln Pro Gly Glu Gln Arg Thr Ile Thr Val Glu Phe Cys Pro Leu  
245 250 255

Lys Arg Gly Arg Val Thr Asn Ile Ala Thr Val Ser Tyr Cys Gly Gly  
260 265 270

His Lys Asn Thr Ala Ser Val Thr Thr Val Ile Asn Glu Pro Cys Val  
275 280 285

Gln Val Asn Ile Glu Gly Ala Asp Trp Ser Tyr Val Cys Lys Pro Val  
290 295 300

Glu Tyr Val Ile Ser Val Ser Asn Pro Gly Asp Leu Val Leu Arg Asp  
305 310 315 320

Val Val Ile Glu Asp Thr Leu Ser Pro Gly Ile Thr Val Val Glu Ala  
325 330 335

Ala Gly Ala Gln Ile Ser Cys Asn Lys Leu Val Trp Thr Leu Lys Glu  
340 345 350

Leu Asn Pro Gly Glu Ser Leu Gln Tyr Lys Val Leu Val Arg Ala Gln  
355 360 365

Thr Pro Gly Gln Phe Thr Asn Asn Val Val Val Lys Ser Cys Ser Asp  
370 375 380

Cys Gly Ile Cys Thr Ser Cys Ala Glu Ala Thr Thr Tyr Trp Lys Gly  
385 390 395 400

Val Ala Ala Thr His Met Cys Val Val Asp Thr Cys Asp Pro Ile Cys  
405 410 415

Val Gly Glu Asn Thr Val Tyr Arg Ile Cys Val Thr Asn Arg Gly Ser  
420 425 430

# APL-03-04PCT\_Sequence\_Listing

Ala Glu Asp Thr Asn Val Ser Leu Ile Leu Lys Phe Ser Lys Glu Leu  
435 440 445

Gln Pro Ile Ser Phe Ser Gly Pro Thr Lys Gly Thr Ile Thr Gly Asn  
450 455 460

Thr Val Val Phe Asp Ser Leu Pro Arg Leu Gly Ser Lys Glu Thr Val  
465 470 475 480

Glu Phe Ser Val Thr Leu Lys Ala Val Ser Ala Gly Asp Ala Arg Gly  
485 490 495

Glu Ala Ile Leu Ser Ser Asp Thr Leu Thr Val Pro Val Ser Asp Thr  
500 505 510

Glu Asn Thr His Ile Tyr  
515

<210> 7  
<211> 1551  
<212> DNA  
<213> Chlamydia trachomatis

<220>  
<221> CDS  
<222> (1)..(1551)

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aaa gac aac act tct cat aaa agc aaa aaa gca aga aaa aac cac agc 96  
Lys Asp Asn Thr Ser His Lys Ser Lys Lys Ala Arg Lys Asn His Ser  
20 25 30  
aaa gag act ccc gta gac cgt aaa gag gtt gct ccg gtt cat gag tct 144  
Lys Glu Thr Pro Val Asp Arg Lys Glu Val Ala Pro Val His Glu Ser  
35 40 45  
aaa gct aca gga cct aaa cag gat tct tgc ttt ggc aga atg tat aca 192  
Lys Ala Thr Gly Pro Lys Gln Asp Ser Cys Phe Gly Arg Met Tyr Thr  
50 55 60  
gtc aaa gtt aat gat gat cgc aat gtt gaa atc aca caa gct gtt cct 240  
Val Lys Val Asn Asp Asp Arg Asn Val Glu Ile Thr Gln Ala Val Pro  
65 70 75 80  
gaa tat gct acg gta gga tct ccc tat cct att gaa att act gct aca 288  
Glu Tyr Ala Thr Val Gly Ser Pro Tyr Pro Ile Glu Ile Thr Ala Thr  
85 90 95  
ggc aaa agg gat tgt gtt gat gtt atc att act cag caa tta cca tgt 336  
Gly Lys Arg Asp Cys Val Asp Val Ile Ile Thr Gln Gln Leu Pro Cys  
100 105 110

# APL-03-04PCT\_Sequence\_Listing

gaa Glu	gca Ala	gag Glu 115	ttc Phe	gta Val	cgc Arg	agt Ser	gat Asp 120	cca Pro	gcg Ala	aca Thr	act Thr	cct Pro 125	act Thr	gct Ala	gat Asp	384
ggt Gly	aag Lys 130	cta Leu	gtt Val	tgg Trp	aaa Lys	att Ile 135	gac Asp	cgc Arg	tta Leu	gga Gly	caa Gln 140	ggc Gly	gaa Glu	aag Lys	agt Ser	432
aaa Lys 145	att Ile	act Thr	gta Val	tgg Trp	gta Val 150	aaa Lys	cct Pro	ctt Leu	aaa Lys	gaa Glu 155	ggt Gly	tgc Cys	tgc Cys	ttt Phe	aca Thr 160	480
gct Ala	gca Ala	aca Thr	gta Val	tgc Cys 165	gct Ala	tgt Cys	cca Pro	gag Glu	atc Ile 170	cg Arg	tcg Ser	gtt Val	aca Thr	aaa Lys 175	tgt Cys	528
gga Gly	caa Gln	cct Pro	gct Ala 180	atc Ile	tgt Cys	gtt Val	aaa Lys	caa Gln 185	gaa Glu	ggc Gly	cca Pro	gag Glu	aat Asn 190	gct Ala	tgt Cys	576
ttg Leu	cg Arg	tgc Cys 195	cca Pro	gta Val	gtt Val	tac Tyr	aaa Lys 200	att Ile	aat Asn	ata Ile	gtg Val	aac Asn 205	caa Gln	gga Gly	aca Thr	624
gca Ala 210	aca Thr	gct Ala	cg Arg	aac Asn	gtt Val 215	gtt Val	gtt Val	gaa Glu	aat Asn	cct Pro	gtt Val 220	cca Pro	gat Asp	ggt Gly	tac Tyr	672
gct Ala 225	cat His	tct Ser	tct Ser	gga Gly 230	cag Gln	cg Arg	gta Val	ctg Leu	acg Thr	ttt Phe 235	act Thr	ctt Leu	gga Gly	gat Asp	atg Met 240	720
caa Gln	cct Pro	gga Gly	gag Glu	cac His 245	aga Arg	aca Thr	att Ile	act Thr	gta Val 250	gag Glu	ttt Phe	tgt Cys	ccg Pro	ctt Leu 255	aaa Lys	768
cg Arg	ggt Gly	cg Arg	gct Ala 260	acc Thr	aat Asn	ata Ile	gca Ala	acg Thr 265	gtt Val	tct Ser	tac Tyr	tgt Cys 270	gga Gly	gga Gly	cat His	816
aaa Lys	aat Asn	aca Thr 275	gca Ala	agc Ser	gta Val	aca Thr	act Thr 280	gtg Val	atc Ile	aac Asn	gag Glu	cct Pro 285	tgc Cys	gta Val	caa Gln	864
gta Val 290	agt Ser	att Ile	gca Ala	gga Gly	gca Ala	gat Asp 295	tgg Trp	tct Ser	tat Tyr	gtt Val	tgt Cys 300	aag Lys	cct Pro	gta Val	gaa Glu	912
tat Tyr 305	gtg Val	atc Ile	tcc Ser	gtt Val	tcc Ser 310	aat Asn	cct Pro	gga Gly	gat Asp	ctt Leu 315	gtg Val	ttg Leu	cga Arg	gat Asp	gtc Val 320	960
gtc Val	gtt Val	gaa Glu	gac Asp	act Thr 325	ctt Leu	tct Ser	ccc Pro	gga Gly	gtc Val 330	aca Thr	gtt Val	ctt Leu	gaa Glu	gct Ala 335	gca Ala	1008
gga Gly	gct Ala	caa Gln	att Ile 340	tct Ser	tgt Cys	aat Asn	aaa Lys	gta Val 345	gtt Val	tgg Trp	act Thr	gtg Val 350	aaa Lys	gaa Glu	ctg Leu	1056
aat Asn	cct Pro	gga Gly	gag Glu	tct Ser	cta Leu	cag Gln	tat Tyr	aaa Lys	gtt Val	cta Leu	gta Val	aga Arg	gca Ala	caa Gln	act Thr	1104



# APL-03-04PCT\_Sequence\_Listing

355	360	365	
cct gga caa ttc aca aat aat gtt gtt gtg aag agc tgc tct gac tgt Pro Gly Gln Phe Thr Asn Asn Val Val Val Lys Ser Cys Ser Asp Cys 370 375 380			1152
ggt act tgt act tct tgc gca gaa gcg aca act tac tgg aaa gga gtt Gly Thr Cys Thr Ser Cys Ala Glu Ala Thr Thr Tyr Trp Lys Gly Val 385 390 395 400			1200
gct gct act cat atg tgc gta gta gat act tgt gac cct gtt tgt gta Ala Ala Thr His Met Cys Val Val Asp Thr Cys Asp Pro Val Cys Val 405 410 415			1248
gga gaa aat act gtt tac cgt att tgt gtc acc aac aga ggt tct gca Gly Glu Asn Thr Val Tyr Arg Ile Cys Val Thr Asn Arg Gly Ser Ala 420 425 430			1296
gaa gat aca aat gtt tct tta atg ctt aaa ttc tct aaa gaa ctg caa Glu Asp Thr Asn Val Ser Leu Met Leu Lys Phe Ser Lys Glu Leu Gln 435 440 445			1344
cct gta tcc ttc tct gga cca act aaa gga acg att aca ggc aat aca Pro Val Ser Phe Ser Gly Pro Thr Lys Gly Thr Ile Thr Gly Asn Thr 450 455 460			1392
gta gta ttc gat tcg tta cct aga tta ggt tct aaa gaa act gta gag Val Val Phe Asp Ser Leu Pro Arg Leu Gly Ser Lys Glu Thr Val Glu 465 470 475 480			1440
ttt tct gta aca ttg aaa gca gta tca gct gga gat gct cgt ggg gaa Phe Ser Val Thr Leu Lys Ala Val Ser Ala Gly Asp Ala Arg Gly Glu 485 490 495			1488
gcg att ctt tct tcc gat aca ttg act gtt cca gtt tct gat aca gag Ala Ile Leu Ser Ser Asp Thr Leu Thr Val Pro Val Ser Asp Thr Glu 500 505 510			1536
aat aca cac atc tat Asn Thr His Ile Tyr 515			1551

<210> 8  
 <211> 517  
 <212> PRT  
 <213> Chlamydia trachomatis

<400> 8

Met Glu Ser Leu Ser Thr Asn Val Ile Ser Leu Ala Asp Thr Lys Ala  
 1 5 10 15

Lys Asp Asn Thr Ser His Lys Ser Lys Lys Ala Arg Lys Asn His Ser  
 20 25 30

Lys Glu Thr Pro Val Asp Arg Lys Glu Val Ala Pro Val His Glu Ser  
 35 40 45

Lys Ala Thr Gly Pro Lys Gln Asp Ser Cys Phe Gly Arg Met Tyr Thr  
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50

55

60

Val Lys Val Asn Asp Asp Arg Asn Val Glu Ile Thr Gln Ala Val Pro  
65 70 75 80

Glu Tyr Ala Thr Val Gly Ser Pro Tyr Pro Ile Glu Ile Thr Ala Thr  
85 90 95

Gly Lys Arg Asp Cys Val Asp Val Ile Ile Thr Gln Gln Leu Pro Cys  
100 105 110

Glu Ala Glu Phe Val Arg Ser Asp Pro Ala Thr Thr Pro Thr Ala Asp  
115 120 125

Gly Lys Leu Val Trp Lys Ile Asp Arg Leu Gly Gln Gly Glu Lys Ser  
130 135 140

Lys Ile Thr Val Trp Val Lys Pro Leu Lys Glu Gly Cys Cys Phe Thr  
145 150 155 160

Ala Ala Thr Val Cys Ala Cys Pro Glu Ile Arg Ser Val Thr Lys Cys  
165 170 175

Gly Gln Pro Ala Ile Cys Val Lys Gln Glu Gly Pro Glu Asn Ala Cys  
180 185 190

Leu Arg Cys Pro Val Val Tyr Lys Ile Asn Ile Val Asn Gln Gly Thr  
195 200 205

Ala Thr Ala Arg Asn Val Val Val Glu Asn Pro Val Pro Asp Gly Tyr  
210 215 220

Ala His Ser Ser Gly Gln Arg Val Leu Thr Phe Thr Leu Gly Asp Met  
225 230 235 240

Gln Pro Gly Glu His Arg Thr Ile Thr Val Glu Phe Cys Pro Leu Lys  
245 250 255

Arg Gly Arg Ala Thr Asn Ile Ala Thr Val Ser Tyr Cys Gly Gly His  
260 265 270

Lys Asn Thr Ala Ser Val Thr Thr Val Ile Asn Glu Pro Cys Val Gln  
275 280 285

Val Ser Ile Ala Gly Ala Asp Trp Ser Tyr Val Cys Lys Pro Val Glu  
290 295 300

# APL-03-04PCT\_Sequence\_Listing

Tyr Val Ile Ser Val Ser Asn Pro Gly Asp Leu Val Leu Arg Asp Val  
305 310 315 320

Val Val Glu Asp Thr Leu Ser Pro Gly Val Thr Val Leu Glu Ala Ala  
325 330 335

Gly Ala Gln Ile Ser Cys Asn Lys Val Val Trp Thr Val Lys Glu Leu  
340 345 350

Asn Pro Gly Glu Ser Leu Gln Tyr Lys Val Leu Val Arg Ala Gln Thr  
355 360 365

Pro Gly Gln Phe Thr Asn Asn Val Val Val Lys Ser Cys Ser Asp Cys  
370 375 380

Gly Thr Cys Thr Ser Cys Ala Glu Ala Thr Thr Tyr Trp Lys Gly Val  
385 390 395 400

Ala Ala Thr His Met Cys Val Val Asp Thr Cys Asp Pro Val Cys Val  
405 410 415

Gly Glu Asn Thr Val Tyr Arg Ile Cys Val Thr Asn Arg Gly Ser Ala  
420 425 430

Glu Asp Thr Asn Val Ser Leu Met Leu Lys Phe Ser Lys Glu Leu Gln  
435 440 445

Pro Val Ser Phe Ser Gly Pro Thr Lys Gly Thr Ile Thr Gly Asn Thr  
450 455 460

Val Val Phe Asp Ser Leu Pro Arg Leu Gly Ser Lys Glu Thr Val Glu  
465 470 475 480

Phe Ser Val Thr Leu Lys Ala Val Ser Ala Gly Asp Ala Arg Gly Glu  
485 490 495

Ala Ile Leu Ser Ser Asp Thr Leu Thr Val Pro Val Ser Asp Thr Glu  
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Asn Thr His Ile Tyr  
515

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<211> 37  
<212> DNA  
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<400> 9  
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# APL-03-04PCT\_Sequence\_Listing

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